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=> file medline hcaplus biosis biotechds scisearch embase
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=> s alcohol dehydrogenase and pyruvate kinase
L1          390 ALCOHOL DEHYDROGENASE AND PYRUVATE KINASE

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2          237 DUP REM L1 (153 DUPLICATES REMOVED)

=> s l2 and dna
L3           34 L2 AND DNA

=> s l3 and 1980-1994/py
   5 FILES SEARCHED...
L4           16 L3 AND 1980-1994/PY

=>  d l4 1-16 ibib ab

L4   ANSWER 1 OF 16     MEDLINE on STN
ACCESSION NUMBER:    94261102      MEDLINE Full-text
DOCUMENT NUMBER:     PubMed ID: 8202080
TITLE:               Open reading frames in the antisense strands of genes
                     coding for glycolytic enzymes in Saccharomyces cerevisiae.
AUTHOR:              Boles E; Zimmermann F K
CORPORATE SOURCE:    Institut fur Mikrobiologie, Technische Hochschule
                     Darmstadt, Germany.
SOURCE:              Molecular & general genetics : MGG, (1994 May 25)
                     243 (4) 363-8.
```

Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199407
ENTRY DATE: Entered STN: 19940714
Last Updated on STN: 19980206
Entered Medline: 19940705

AB Open reading frames longer than 300 bases were observed in the antisense strands of the genes coding for the glycolytic enzymes phosphoglucose isomerase, phosphoglycerate mutase, **pyruvate kinase** and **alcohol dehydrogenase** I. The open reading frames on both strands are in codon register. It has been suggested that proteins coded in codon register by complementary **DNA** strands can bind to each other. Consequently, it was interesting to investigate whether the open reading frames in the antisense strands of glycolytic enzyme genes are functional. We used oligonucleotide-directed mutagenesis of the PGI1 phosphoglucose isomerase gene to introduce pairs of closely spaced base substitutions that resulted in stop codons in one strand and only silent replacements in the other. Introduction of the two stop codons into the PGI1 sense strand caused the same physiological defects as already observed for pgi1 deletion mutants. No detectable effects were caused by the two stop codons in the antisense strand. A deletion that removed a section from -31 bp to +109 bp of the PGI1 gene but left 83 bases of the 3' region beyond the antisense open reading frame had the same phenotype as a deletion removing both reading frames. A similar pair of deletions of the PYK1 gene and its antisense reading frame showed identical defects. Our own Northern experiments and those reported by other authors using double-stranded probes detected only one transcript for each gene. These observations indicate that the antisense reading frames are not functional. On the other hand, evidence is provided to show that the rather long reading frames in the antisense strands of these glycolytic enzyme genes could arise from the strongly selective codon usage in highly expressed yeast genes, which reduces the frequency of stop codons in the antisense strand.

L4 ANSWER 2 OF 16 MEDLINE on STN
ACCESSION NUMBER: 94011314 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 8406815
TITLE: Glycolytic enzymes of Candida albicans are nonubiquitous immunogens during candidiasis.
AUTHOR: Swoboda R K; Bertram G; Hollander H; Greenspan D; Greenspan J S; Gow N A; Gooday G W; Brown A J
CORPORATE SOURCE: Marischal College, University of Aberdeen, United Kingdom.
SOURCE: Infection and immunity, **(1993 Oct)** 61 (10) 4263-71.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; AIDS
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19940117
Entered Medline: 19931116

AB A cDNA library was made with mRNA from Candida albicans grown under conditions favoring the hyphal form. The library was screened for sequences that encode immunogenic proteins by using pooled sera from five patients with oral candidiasis and five uninfected patients. Most of these patients were human immunodeficiency virus positive. From 40,000 cDNA clones screened, 83

positive clones were identified. Of these, 10 clones were chosen at random for further analysis. None of these 10 cDNAs were derived from a multigene family. The 5' and 3' ends of all 10 clones were analyzed by **DNA** sequencing. Two cDNAs were separate isolates of a sequence with strong homology to **pyruvate kinase** genes from other fungi (59 to 73%) and humans (60%). A third cDNA had strong sequence homology to the Saccharomyces cerevisiae and Kluyveromyces lactis **alcohol dehydrogenase** genes (68 to 73%). A fourth cDNA was homologous (81%) to an S. cerevisiae protein of unknown function. The functions of the remaining six C. albicans cDNAs are not known. A more detailed analysis of the clones encoding glycolytic enzymes revealed that sera from few patients recognized them as antigens. Therefore, although glycolytic enzymes constitute a group of C. albicans proteins that are immunogenic during oral and esophageal infections, their detection cannot be exploited as an accurate marker of infection.

L4 ANSWER 3 OF 16 MEDLINE on STN
ACCESSION NUMBER: 91176551 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 2127735
TITLE: The **DNA**-binding protein RAP1 is required for efficient transcriptional activation of the yeast PYK glycolytic gene.
AUTHOR: McNeil J B; Dykshoorn P; Huy J N; Small S
CORPORATE SOURCE: Department of Microbiology, University of Toronto, Ontario, Canada.
SOURCE: Current genetics, **(1990 Dec)** 18 (5) 405-12.
Journal code: 8004904. ISSN: 0172-8083.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199104
ENTRY DATE: Entered STN: 19910519
Last Updated on STN: 20000303
Entered Medline: 19910430

AB We show by deletion mutagenesis, followed by in vivo and in vitro analysis, that the binding of a protein factor to the upstream activation sequence (UAS) of the Saccharomyces cerevisiae glycolytic gene PYK, encoding **pyruvate kinase**, is required for efficient transcription of the corresponding coding region. In addition, gel electrophoretic mobility shift and DNase I protection studies, involving yeast gene products expressed in E. coli, suggest that this trans-acting **DNA**-binding protein is encoding by the RAP1 gene. The identification of RAP1 binding sites located within the UAS element of the yeast PYK, PGK (phosphoglycerate kinase) and ENO1 (enolase) genes, and in the 5'-upstream region of the ADHI (**alcohol dehydrogenase**) gene, suggests that a mechanism of coordinate gene expression involving several of the glycolytic genes may exist in yeast.

L4 ANSWER 4 OF 16 MEDLINE on STN
ACCESSION NUMBER: 89008102 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 2844728
TITLE: Changes in activities of several enzymes involved in carbohydrate metabolism during the cell cycle of Saccharomyces cerevisiae.
AUTHOR: Van Doorn J; Valkenburg J A; Scholte M E; Oehlen L J; Van Driel R; Postma P W; Nanninga N; Van Dam K
CORPORATE SOURCE: Laboratory of Biochemistry and Biotechnology Centre, University of Amsterdam, The Netherlands.
SOURCE: Journal of bacteriology, **(1988 Oct)** 170 (10)

4808-15.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198811
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19900308
Entered Medline: 19881114

AB Activity changes of a number of enzymes involved in carbohydrate metabolism were determined in cell extracts of fractionated exponential-phase populations of Saccharomyces cerevisiae grown under excess glucose. Cell-size fractionation was achieved by an improved centrifugal elutriation procedure. Evidence that the yeast populations had been fractionated according to age in the cell cycle was obtained by examining the various cell fractions for their volume distribution and their microscopic appearance and by flow cytometric analysis of the distribution patterns of cellular **DNA** and protein contents. Trehalase, hexokinase, **pyruvate kinase**, phosphofructokinase 1, and fructose-1,6-diphosphatase showed changes in specific activities throughout the cell cycle, whereas the specific activities of **alcohol dehydrogenase** and glucose-6-phosphate dehydrogenase remained constant. The basal trehalase activity increased substantially (about 20-fold) with bud emergence and decreased again in binucleated cells. However, when the enzyme was activated by pretreatment of the cell extracts with cyclic AMP-dependent protein kinase, no significant fluctuations in activity were seen. These observations strongly favor posttranslational modification through phosphorylation-dephosphorylation as the mechanism underlying the periodic changes in trehalase activity during the cell cycle. As observed for trehalase, the specific activities of hexokinase and phosphofructokinase 1 rose from the beginning of bud formation onward, finally leading to more than eightfold higher values at the end of the S phase. Subsequently, the enzyme activities dropped markedly at later stages of the cycle. **Pyruvate kinase** activity was relatively low during the G1 phase and the S phase, but increased dramatically (more than 50-fold) during G2. In contrast to the three glycolytic enzymes investigated, the highest specific activity of the gluconeogenic enzyme fructose-1, 6-diphosphatase 1 was found in fractions enriched in either unbudded cells with a single nucleus or binucleated cells. The observed changes in enzyme activities most likely underlie pronounced alterations in carbohydrate metabolism during the cell cycle.

L4 ANSWER 5 OF 16 MEDLINE on STN
ACCESSION NUMBER: 88113473 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 3276589
TITLE: Long-term culture of hepatocytes: effect of hormones on enzyme activities and metabolic capacity.
AUTHOR: Dich J; Vind C; Grunnet N
CORPORATE SOURCE: Department of Biochemistry A, Panum Institute, University of Copenhagen, Denmark.
SOURCE: Hepatology (Baltimore, Md.), **(1988 Jan-Feb)** 8 (1) 39-45.
Journal code: 8302946. ISSN: 0270-9139.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198803
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19900308

Entered Medline: 19880307

AB (i) Hepatocytes isolated from adult rats were cultured for 2 to 3 weeks on collagen in a modified, serum-free Waymouth medium containing fatty acids and varying concentrations of glucocorticoid, insulin and glucagon. (ii) In the presence of all three hormones, it was possible to maintain the content of **DNA**, the activity of glucokinase, **pyruvate kinase**, hexokinase and lactate dehydrogenase at initial levels for 2 to 3 weeks. The activity of glucokinase and **pyruvate kinase** was affected by the concentration of insulin. (iii) The activity of **alcohol dehydrogenase** was stable for 3 days and declined to about 25% of the initial level after 2 weeks of culture, irrespective of the presence of hormones. (iv) Maintenance of albumin secretion was dependent on the presence of glucocorticoid, and glucocorticoid and insulin showed an additive or, at some time points, a synergistic effect on its secretion. (v) The content of cytochrome P-450 could be kept at 65% of the initial level, provided that a relatively high concentration of dexamethasone was present (10(-6) M). (vi) In the absence of hormones, urea synthesis was 70% of initial levels throughout the experimental period. With insulin and glucocorticoid present, a high concentration of glucagon (10(-8) M) was required to maintain the synthesis of urea at this level. (vii) It is concluded that hepatocyte cultures as described in the present study may be a useful, well-defined system for long-term metabolic, pharmacologic and toxicologic studies.

L4 ANSWER 6 OF 16 MEDLINE on STN

ACCESSION NUMBER: 88106799 MEDLINE Full-text

DOCUMENT NUMBER: PubMed ID: 3322306

TITLE: Long-term culture of hepatocytes: ethanol oxidation and effect of ethanol on enzyme activities and albumin secretion.

AUTHOR: Dich J; Vind C; Grunnet N

CORPORATE SOURCE: Department of Biochemistry A, Panum Institute, University of Copenhagen, Denmark.

SOURCE: Alcohol and alcoholism (Oxford, Oxfordshire), **(1987)** Suppl 1 271-5.
Journal code: 8310684. ISSN: 0735-0414.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198803

ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19980206
Entered Medline: 19880323

AB Rat hepatocytes were cultured in a modified HI-WO/BA medium for 13 days, and the combined effect of dexamethasone, 10(-7) M, insulin, 10(-8) M, and glucagon, 10(-9) M on the **DNA**-content, and on the activity of several enzymes, the secretion of albumin and the rate of ethanol oxidation was investigated. The effect of ethanol on these parameters was also studied. All parameters measured declined with time in the hormone-free cultures. In hormone-supplemented cultures, the **DNA** -content, the activity of glucokinase, **pyruvate kinase** , hexokinase and lactate dehydrogenase and the secretion of albumin was maintained at reasonable levels throughout the 13 days, whereas both the activity of **alcohol dehydrogenase** and the rate of ethanol oxidation fell significantly, although less than in hormone-free cultures. Addition of 50 mM ethanol to the hormone-supplemented culture medium caused a ca. 20% fall in the activity of glucokinase and **pyruvate kinase** and a 20% increase in **alcohol dehydrogenase** activity. No effect of ethanol was observed on the activity of hexokinase and lactate dehydrogenase or on the secretion of albumin.

L4 ANSWER 7 OF 16 MEDLINE on STN
ACCESSION NUMBER: 86176703 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 2938077
TITLE: Intron-dependent evolution of the nucleotide-binding domains within **alcohol dehydrogenase** and related enzymes.
AUTHOR: Duester G; Jornvall H; Hatfield G W
CONTRACT NUMBER: AA-06622 (NIAAA)
GM-08733 (NIGMS)
GM-32112 (NIGMS)
SOURCE: Nucleic acids research, **(1986 Mar 11)** 14 (5) 1931-41.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198604
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19990129
Entered Medline: 19860425

AB It has been suggested that the intron/exon structure of a gene corresponds to its evolutionary history. Accordingly, early in evolution **DNA** segments encoding short functional polypeptides may have been rearranged (exon-shuffling) to create full-length genes and RNA splicing may have been developed to remove intervening sequences (introns) in order to preserve translational reading frames. A conflicting viewpoint would be that introns were randomly inserted into previously uninterrupted genes after their initial evolutionary development. If so, the sites of introns would be unlikely to consistently reflect the domain structure of the protein. To address this question, the intron/exon structure of the gene encoding human **alcohol dehydrogenase** (ADH) was determined and compared to the gene structures for other ADHs and related proteins, all of which possess nucleotide-binding domains. Our results indicate that the introns in the nucleotide-binding domains of all the genes examined do indeed fall at positions which separate the short functional polypeptides (i.e. beta strands) which are believed to comprise this domain. We argue that our data is most easily explained by the hypothesis that introns were present in an ancestral nucleotide-binding domain which was later rearranged by exon-shuffling to form the various dehydrogenases and kinases which utilize such a domain.

L4 ANSWER 8 OF 16 MEDLINE on STN
ACCESSION NUMBER: 85099332 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 2981634
TITLE: Intron/exon structure of the chicken **pyruvate kinase** gene.
AUTHOR: Lonberg N; Gilbert W
CONTRACT NUMBER: GM09541-22 (NIGMS)
SOURCE: Cell, **(1985 Jan)** 40 (1) 81-90.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M10619; GENBANK-M10782; GENBANK-M18788; GENBANK-M18789; GENBANK-M18790; GENBANK-M18791; GENBANK-M18792; GENBANK-M18793
ENTRY MONTH: 198502
ENTRY DATE: Entered STN: 19900320

Last Updated on STN: 19970203
Entered Medline: 19850225

AB The chicken **pyruvate kinase** gene is interrupted by at least ten introns, including nine introns within the coding region. We compare the structure of this gene with the three-dimensional protein structure of the homologous cat muscle enzyme. The introns are not randomly placed--they divide the coding sequence into fairly uniformly sized pieces encoding discrete elements of secondary structure. The introns tend to fall at interruptions between stretches of alpha-helix or beta-sheet residues, and each of the six exons that contribute to the barrel-shaped central domain include one or two repeats of a simple unit, an alpha-helix plus a beta strand. This structure suggests that introns were not inserted into a previously uninterrupted coding sequence, but instead are products of the evolution of the first **pyruvate kinase** gene. We have found some sequence homology between a segment of **pyruvate kinase** and the structurally homologous mononucleotide binding fold of **alcohol dehydrogenase.** The superposition of these two regions aligns an intron from the maize **alcohol dehydrogenase** gene four nucleotides from an intron in the chicken **pyruvate kinase** gene.

L4 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:75650 HCAPLUS Full-text
DOCUMENT NUMBER: 120:75650
TITLE: Manufacture of soluble metabolic products using transformed algae
INVENTOR(S): Moll, Benjamin A.
PATENT ASSIGNEE(S): DNA Plant Technology Corp., USA
SOURCE: U.S., 15 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5270175	A	19931214	US 1991-729513	19910712 <--

PRIORITY APPLN. INFO.: US 1991-729513 19910712

AB Soluble metabolic products, such as ethanol, are produced by growing modified algal cells in a growth medium and recovering the products from the growth medium. The algal cells are modified to overproduce the metabolic product by providing for overexpression of at least one enzyme in the metabolic pathway for the product. For the production of ethanol, the alc. dehydrogenase gene, the pyruvate decarboxylase gene, or both, are overexpressed, typically under the control of a heterologous promoter. The algal cells may be modified by transformation with a **DNA** construct including coding sequence(s) of the enzyme(s) under the control of a heterologous promoter.

L4 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1989:474192 HCAPLUS Full-text
DOCUMENT NUMBER: 111:74192
TITLE: Correlation between internal motion and emission kinetics of tryptophan residues in proteins
AUTHOR(S): Kouyama, Tsutomu; Kinosita, Kazuhiko, Jr.; Ikegami, Akira
CORPORATE SOURCE: Inst. Phys. Chem. Res., Wako, 351-01, Japan
SOURCE: European Journal of Biochemistry (**1989**), 182(3), 517-21

CODEN: EJBCAI; ISSN: 0014-2956
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Time-resolved fluorescence anisotropy measurements of tryptophan residues were done for 44 proteins. Internal rotational motion with a sub-nanosecond correlation time (0.9 ns at 10°) was seen in a large number of proteins, though its amplitude varied from protein to protein. Tryptophan residues that were almost fixed within a protein had either a long (>4 ns) or short (<2 ns) fluorescence lifetime, whereas a residue undergoing a large internal motion had an intermediate lifetime (1.5-3 ns). It is suggested that the emission kinetics of a tryptophan residue is coupled with its internal motion. An immobile tryptophan residue emitting at long wavelength was characterized by a long lifetime (>4 ns). It appears that a tryptophan residue fixed in a polar region has little change of being quenched by neighboring groups.

L4 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1989:90866 HCAPLUS Full-text
DOCUMENT NUMBER: 110:90866
TITLE: Biological implications of complementary hydropathy of amino acids
AUTHOR(S): Brentani, Ricardo R.
CORPORATE SOURCE: Sao Paulo Branch, Ludwig Inst. Cancer Res., Sao Paulo, 01509, Brazil
SOURCE: Journal of Theoretical Biology (1988), 135(4), 495-9
CODEN: JTBIAP; ISSN: 0022-5193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The principle of complementary hydropathy predicts that peptides coded for by opposing **DNA** strands will bind one another because highly hydrophilic amino acids will be complemented by hydrophobic ones and vice versa. This paper provides the chemical plausibility for such interactions. It is suggested that exons coding for interacting proteins were juxtaposed and co-evolved together. Present day genes are no longer thus arranged because of duplications and exon shuffling.

L4 ANSWER 12 OF 16 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1987:35601 BIOSIS Full-text
DOCUMENT NUMBER: PREV198732015689; BR32:15689
TITLE: LONG-TERM CULTURE OF HEPATOCYTES THE ACTIVITY OF ENZYMES.
AUTHOR(S): DICH J [Reprint author]; VIND C; GRUNNET N
CORPORATE SOURCE: DEP BIOCHEMISTRY A, PANUM INST, UNIV COPENHAGEN, DENMARK
SOURCE: Alcohol and Alcoholism, (1986) Vol. 21, No. 2, pp. A24.
Meeting Info.: THIRD CONGRESS OF THE INTERNATIONAL SOCIETY FOR BIOMEDICAL RESEARCH ON ALCOHOLISM, HELSINKI, FINLAND, JUNE 8-13. 1986. ALCOHOL ALCOHOL.
CODEN: ALALDD. ISSN: 0735-0414.
DOCUMENT TYPE: Conference; (Meeting)
FILE SEGMENT: BR
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 22 Dec 1986
Last Updated on STN: 22 Dec 1986

L4 ANSWER 13 OF 16 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
ACCESSION NUMBER: 1992-02493 BIOTECHDS
TITLE: Use of yeast glyceraldehyde-3-phosphate-dehydrogenase promoter for new vector construction;
for high-level production of e.g. hepatitis B virus

surface antigen in yeast
PATENT ASSIGNEE: Chiron
PATENT INFO: EP 460716 **11 Dec 1991**
APPLICATION INFO: EP 1984-114001 6 Jan 1984
PRIORITY INFO: US 1983-468589 22 Mar 1983
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1991-363206 [50]
AB A yeast expression vector comprising a segment of foreign **DNA** under transcriptional control of a yeast glyceraldehyde-3-phosphate- dehydrogenase (GAPDH) promoter, the segment being in the correct orientation for transcription and having 3 or fewer codons from yeast GAPDH at the 5' end of the foreign **DNA**, and where the foreign **DNA** encodes hepatitis B virus surface antigen (HBsAg), is claimed. The expression vector may also comprise a yeast replication origin (for vector expression in yeast) or a bacterial replication origin (for expression in bacteria), and a terminator attached to the 3' end of the foreign **DNA.** The terminator may be a yeast **alcohol - dehydrogenase**-I, GAPDH or **pyruvate-kinase** terminator. The vector may also include **DNA** from the yeast plasmid 2-um. Also claimed is a method of expressing a **DNA** coding segment in yeast comprising (a) inserting the segment in a yeast expression vector, and (b) transforming yeast cells with the coding segment expression vector. The yeast GAPDH promoter has high efficiency and can be used to produce large amounts of foreign protein, especially HBsAg. (10pp)

L4 ANSWER 14 OF 16 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
ACCESSION NUMBER: 1989-13723 BIOTECHDS
TITLE: Yeast vectors for expressing hepatitis B surface antigen; under control of high efficiency **pyruvate-kinase** promoter
PATENT ASSIGNEE: Chiron
PATENT INFO: EP 329203 **23 Aug 1989**
APPLICATION INFO: EP 1984-106868 6 Jan 1984
PRIORITY INFO: US 1982-468589 22 Feb 1982
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1989-243119 [34]
AB New yeast expression vectors comprise a segment of foreign **DNA** (I) in the correct orientation for transcription and under control of the yeast **pyruvate-kinase** (PK, EC-2.7.1.40) promoter, and contain less than 3 codons from yeast PK at the 5' end of (I). (I) encodes hepatitis B virus surface antigen (HBsAg), or part of it. A terminator is attached to the 3' end of (I) and the vector includes at least part of the yeast plasmid 2-um **DNA** (ATCC 20666), and optionally also a bacterial origin of replication for replication in yeast and bacteria (e.g. Escherichia coli). The terminator is from the yeast **alcohol-dehydrogenase** (EC-1.1.1.1), glyceraldehyde-3-phosphate-dehydrogenase (EC-1.2.1.12) or PK genes. Yeast cells transformed with these vectors will express large amounts of HBsAg since the specified promoter is very efficient. (15pp)

L4 ANSWER 15 OF 16 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
ACCESSION NUMBER: 1987-07792 BIOTECHDS Full-text
TITLE: Antigenicity and immunogenicity of domains of the human immunodeficiency virus (HIV) envelope polypeptide expressed in the yeast Saccharomyces cerevisiae; potential subunit vaccine development
AUTHOR: Barr P J; Steimer K S; Sabin E A; Parkes D; George-Nascimento C; Stephans J C

CORPORATE SOURCE: Chiron
LOCATION: Chiron Corporation, 4560 Horton Street, Emeryville, CA 94608, USA.
SOURCE: Vaccine; (1987) 5, 2, 90-101
CODEN: VACCDE
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The envelope glycoproteins of human immunodeficiency virus (HIV) are candidates for subunit AIDS vaccines. The production of polypeptides representing regions of the HIV-SF2 envelope gene in genetically engineered yeast is described. Expression vectors were constructed using **DNA** encoding regions env-1, env-2 and env-3 from plasmids containing the HIV-SF2 genome. The regions were cloned with synthetic oligonucleotide adapters containing in-frame initiation and termination codons into the vectors. The vectors contained the yeast glycolytic enzyme promoters for glyceraldehyde- 3-phosphate-dehyrogenase (GAPDH), **pyruvate-kinase** (EC-2.7.1.40) and a glucose regulatable **alcohol-dehydrogenase**-2/GAPDH hybrid promoter. The polypeptides expressed in Saccharomyces cerevisiae representing gp120 and gp41 reacted with antibodies in sera from HIV seropositive humans. The env polypeptides isolated from yeast elicited immune responses in heterologous hosts. Recombinant polypeptides from the gp120 and gp41 coding regions of env were used to raise antibodies in animals. (46 ref)

L4 ANSWER 16 OF 16 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 92:119405 SCISEARCH Full-text
THE GENUINE ARTICLE: HE607
TITLE: ALTERNATIVE SPLICING OF FRUCTOSE-1,6-BISPHOSPHATE ALDOLASE TRANSCRIPTS IN DROSOPHILA-MELANOGASTER PREDICTS 3 ISOZYMES
AUTHOR: SHAWLEE R; LISSEMORE J L; SULLIVAN D T; TOLAN D R (Reprint)
CORPORATE SOURCE: BOSTON UNIV, DEPT BIOL, 5 CUMMINGTON ST, BOSTON, MA, 02215; SYRACUSE UNIV, DEPT BIOL, SYRACUSE, NY, 13244
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (25 **FEB 1992**)
Vol. 267, No. 6, pp. 3959-3967.
ISSN: 0021-9258.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 54

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The genes that encode fructose 1,6-bisphosphate aldolase of Drosophila melanogaster have been isolated and characterized. These genes exist in a single copy 8-kilobase pair locus in the Drosophila genome which is located at cytogenetic position 97A-B. The nucleotide sequence and transcript mapping suggest that three overlapping protein isozyme genes may be encoded at this locus. These isozyme genes all share a single promoter, a 5'-untranslated first exon, and two other protein coding exons. The isozyme-specific carboxyl-terminal amino acids are encoded by one of three alternatively utilized fourth exons: 4A, 4B, or 4C by alternative splicing. The transcript containing exon 4C, whose sequence has been reported previously, is abundant throughout development and has a developmental profile similar to other glycolytic gene transcripts; however, it shows developmental specificity in the alternative use of two polyadenylation signals which result in a 2.4-kilobase and a 1.9-kilobase transcript. The transcript containing exon 4B is 1.6 kilobases in size and is most abundant during the larval stages and during the time of eclosion. The transcript containing exon4A is in low abundance and found only during the adult stage. Sequence comparisons of the alternative fourth exons indicate that

the duplication leading to the multiple exons is quite old and preceded the origin of the genus Drosophila.

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=> d his

     (FILE 'HOME' ENTERED AT 13:23:18 ON 15 APR 2004)

     FILE 'MEDLINE, HCAPLUS, BIOSIS, BIOTECHDS, SCISEARCH, EMBASE' ENTERED AT
     13:24:08 ON 15 APR 2004
L1           390 S ALCOHOL DEHYDROGENASE AND PYRUVATE KINASE
L2           237 DUP REM L1 (153 DUPLICATES REMOVED)
L3            34 S L2 AND DNA
L4            16 S L3 AND 1980-1994/PY

=> log y
COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                34.92      35.34

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     (FILE 'HOME' ENTERED AT 13:44:32 ON 15 APR 2004)

     FILE 'MEDLINE, HCAPLUS, BIOSIS, BIOTECHDS, EMBASE, SCISEARCH' ENTERED AT
     13:45:25 ON 15 APR 2004
L1            75 S PYRUVATE DECARBOXYLASE AND ALCOHOL DEHYDROGENASE AND DNA
L2            59 DUP REM L1 (16 DUPLICATES REMOVED)
L3             1 S L2 AND ANIMAL CELL?
L4            59 FOCUS L2 1-
L5            13 S L4 AND 1975-1994/PY

=> s polysaccharase and alcohol dehydrogenase and dna
L6             1 POLYSACCHARASE AND ALCOHOL DEHYDROGENASE AND DNA

=> d l6 ibib ab

L6    ANSWER 1 OF 1  BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
ACCESSION NUMBER: 1994-07006  BIOTECHDS
TITLE:            Ethanol production from an oligosaccharide-containing biomass
      ;
                     using a first stage to produce simpler oligosaccharides
                     and a fermentation stage with recombinant microorganisms
PATENT ASSIGNEE:  Bioenergy-Int.
PATENT INFO:      WO 9406924 31 Mar 1994
APPLICATION INFO: WO 1993-US8558 17 Sep 1993
PRIORITY INFO:    US 1993-26051 5 Mar 1993; US 1992-946290 17 Sep 1992
DOCUMENT TYPE:    Patent
LANGUAGE:         English
OTHER SOURCE:     WPI: 1994-118473 [14]
AB     A new method for ethanol production from oligosaccharide-containing biomass
       involves: (1) contacting the biomass at 50-55 deg and at pH 4.5-5.0 with a
       cellulase (EC-3.2.1.4) to form oligosaccharides and/or monosaccharides; (2)
       producing from the product of (1) a sugar solution containing at least
       glucose, other cellulose-derived sugars and hemicellulose-derived sugars; (3)
       reacting the sugar solution so as to consume part of the sugar solution
       biologically to give a reaction product stream (A) and a depleted sugar
       solution (B); (4) introducing (B) into a fermentor containing recombinant
       microorganisms (containing DNA encoding Zymomonas mobilis alcohol-
       dehydrogenase (EC-1.1.1.1) and pyruvate-decarboxylase (EC-4.1.1.1) and
       optionally also a polysaccharase), preferably Erwinia, Klebsiella or
       Xanthomonas, especially Klebsiella oxytoca M5A1(plasmid pLOI555) (ATCC
       68564); and (5) fermenting (B) at 35 deg and pH 6.0 to give ethanol.  In a
       modified method, the biomass is contacted at 50-60 deg and pH 4.5-5.0 with a
       polysaccharase (a cellulolytic enzyme, a xylanolytic enzyme or a starch-
       degrading enzyme) in step (1).  (172pp)



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     (FILE 'HOME' ENTERED AT 13:44:32 ON 15 APR 2004)

     FILE 'MEDLINE, HCAPLUS, BIOSIS, BIOTECHDS, EMBASE, SCISEARCH' ENTERED AT
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L1            75 S PYRUVATE DECARBOXYLASE AND ALCOHOL DEHYDROGENASE AND DNA
L2            59 DUP REM L1 (16 DUPLICATES REMOVED)
L3             1 S L2 AND ANIMAL CELL?
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L4	59	FOCUS L2 1-
L5	13	S L4 AND 1975-1994/PY
L6	1	S POLYSACCHARASE AND ALCOHOL DEHYDROGENASE AND DNA

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L5: Entry 1 of 1 File: USPT Jan 9, 1996

US-PAT-NO: 5482846
DOCUMENT-IDENTIFIER: US 5482846 A

TITLE: Ethanol production in Gram-positive microbes

DATE-ISSUED: January 9, 1996

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ingram; Lonnie O'Neal	Gainesville	FL		
Barbosa-Alleyne; Maria D. F.	Gainesville	FL		

US-CL-CURRENT: 435/161; 257/E21.317, 435/163, 435/252.31

CLAIMS:

We claim:

1. A Gram-positive bacterium selected from the group consisting of Bacillus subtilis and Bacillus polymyxa which has been transformed with Zymomonas mobilis genes encoding alcohol dehydrogenase and pyruvate decarboxylase, wherein said genes are expressed at sufficient levels to confer upon said Gram-positive bacterium transformant the ability to produce ethanol as a fermentation product.

2. A method for the production of ethanol, said method comprising:

a) transforming a Gram-positive bacterial host selected from the group consisting of Bacillus subtilis and Bacillus polymyxa with Zymomonas mobilis genes encoding alcohol dehydrogenase and pyruvate decarboxylase, wherein said genes are expressed at sufficient levels to result in production of ethanol as a fermentation product, and

b) growing said bacterial host so that ethanol is produced.

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L6: Entry 1 of 1 File: USPT Jun 29, 1999

US-PAT-NO: 5916787
DOCUMENT-IDENTIFIER: US 5916787 A

TITLE: Ethanol production in gram-positive microbes

DATE-ISSUED: June 29, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ingram; Lonnie O'Neal	Gainesville	FL		
Barbosa-Alleyne; Maria D. F.	Gainesville	FL		

US-CL-CURRENT: 435/161; 257/E21.317, 435/162, 435/163, 435/165, 435/252.31, 435/320.1

CLAIMS:

We claim:

1. A Gram-positive bacterium which has been transformed with heterologous genes encoding alcohol dehydrogenase and pyruvate decarboxylase wherein said genes are expressed at sufficient levels to confer upon said Gram-positive bacterium transformant the ability to produce ethanol as a fermentation product.

2. The Gram-positive bacterium, according to claim 1, wherein said host is selected from the group consisting of Bacillus, Lactobacillus, Streptococcus, Fibribacter, Ruminococcus, Pediococcus, Cytophaga, Cellulomonas, Bacteroides, and Clostridium.

3. The Gram-positive bacterium according to claim 2, wherein said host is a Bacillus sp.

4. The Gram-positive bacterium, according to claim 3, wherein said Bacillus sp. is selected from the group consisting of B. subtilis and B. polymyxa.

5. The Gram-positive bacterium, according to claim 1, which has been transformed with Z. mobilis genes encoding alcohol dehydrogenase and pyruvate decarboxylase.

6. The Gram-positive bacterium according to claim 1, wherein said bacterium is further transformed with a gene encoding an enzyme which degrades oligosaccharides.

7. The Gram-positive bacterium, according to claim 6, wherein said enzyme which degrades oligosaccharides is a polysaccharase.

8. The Gram-positive bacterium according to claim 7, wherein said polysaccharase is selected from the group consisting of cellulolytic, xylanolytic, and starch-degrading enzymes.

9. The Gram-positive bacterium, according to claim 1, wherein said heterologous genes are incorporated onto the chromosome of said bacterium.

10. A method for the production of ethanol, said method comprising transforming a Gram-positive bacterial host with heterologous genes encoding pyruvate decarboxylase and alcohol dehydrogenase wherein said genes are expressed at sufficient levels to result in the production of ethanol as a fermentation product.

11. The method, according to claim 10, wherein said host is selected from the group consisting of Bacillus, Lactobacillus, Streptococcus, Fibribacter, Ruminococcus, Pediococcus, Cytophaga, Cellulomonas, Bacteroides, and Clostridium.

12. The method, according to claim 11, wherein said host is a Bacillus sp.

13. The method, according to claim 12, wherein said Bacillus sp. is selected from the group consisting of B. subtilis and B. polymyxa.

14. The method, according to claim 10, wherein said Gram-positive bacterium has been transformed with Z. mobilis genes encoding alcohol dehydrogenase and pyruvate decarboxylase.

15. The method, according to claim 10, wherein said bacterium is further transformed with a gene encoding an enzyme which degrades oligosaccharides.

16. The method, according to claim 15, wherein said enzyme which degrades oligosaccharides is a polysaccharase.

17. A method for reducing the accumulation of acidic metabolic products in the growth medium of Gram-positive bacteria, said method comprising transforming said bacteria with heterologous genes which express alcohol dehydrogenase and pyruvate decarboxylase at sufficient levels to result in the production of ethanol as a fermentation product.

18. A plasmid designated pLOI1500.

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L2: Entry 1 of 1 File: USPT Mar 19, 1991

US-PAT-NO: 5000000
DOCUMENT-IDENTIFIER: US 5000000 A

TITLE: Ethanol production by Escherichia coli strains co-expressing Zymomonas PDC and ADH genes

DATE-ISSUED: March 19, 1991

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ingram; Lonnie O.	Gainesville	FL		
Conway; Tyrrell	Lincoln	NE		
Alterthum; Flavio	Gainesville	FL		

US-CL-CURRENT: 435/161; 257/E21.317, 435/170, 435/252.3, 435/252.33, 435/320.1, 435/488

CLAIMS:

We claim:

1. An Escherichia coli, which has been transformed with Zymomonas mobilis genes coding for alcohol dehydrogenase and pyruvate decarboxylase wherein said genes are expressed at sufficient levels to confer upon said Escherichia coli transformant the ability to produce ethanol as a fermentation product.

2. The Escherichia coli, according to claim 1, wherein the Escherichia coli, prior to transformation, is selected from the group consisting of ATCC 8677, ATCC 8739, ATCC 9637, ATCC 11303, ATCC 11775, ATCC 14948, ATCC 15224, and ATCC 23227.

3. The Escherichia coli, according to claim 1, wherein said Escherichia coli has been transformed with a plasmid selected from the group consisting of pLOI308-10, pLOI297, and pLOI308-11.

4. The Escherichia coli, according to claim 3, wherein said Escherichia coli has been transformed with pLOI297.

5. A method for the production of ethanol, said method comprising transforming an Escherichia coli with Zymomonas mobilis genes coding for pyruvate decarboxylase and alcohol dehydrogenase wherein said genes are expressed by the transformed Escherichia coli at sufficient levels to result in the production of ethanol as a fermentation product when said Escherichia coli is grown in an appropriate medium.

6. The method, according to claim 5, wherein said Escherichia coli is transformed with a plasmid

selected from the group consisting of pLOI308-10, pLOI297, and pLOI308-11.

7. The method, according to claim 6, wherein said Escherichia coli has been transformed with pLOI297.

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L3: Entry 1 of 1 File: USPT Jun 13, 1995

US-PAT-NO: 5424202
DOCUMENT-IDENTIFIER: US 5424202 A

TITLE: Ethanol production by recombinant hosts

DATE-ISSUED: June 13, 1995

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ingram; Lonnie O.	Gainesville	FL		
Beall; David S.	Gainesville	FL		
Burchhardt; Gerhard F. H.	Gainesville	FL		
Guimaraes; Walter V.	Vicosa			BR
Ohta; Kazuyoshi	Miyazaki			JP
Wood; Brent E.	Gainesville	FL		
Shanmugam; Keelnatham T.	Gainesville	FL		

US-CL-CURRENT: 435/161; 257/E21.317, 435/165, 435/252.3, 435/320.1, 435/847, 435/854

CLAIMS:

What is claimed is:

1. A gram negative recombinant host, other than Escherichia coli, comprising a first heterologous DNA coding for alcohol dehydrogenase and pyruvate decarboxylase, wherein said host expresses said heterologous DNA at a sufficient functional level so as to facilitate the production of ethanol as a primary fermentation product by said host.

2. The recombinant host according to claim 1, wherein said host is selected from the group consisting of enteric bacteria.

3. The recombinant host according to claim 2, selected from the group consisting of Erwinia and Klebsiella.

4. The recombinant host according to claim 3, having the ethanol producing characteristics of Klebsiella oxytoca M5A1(pLOI555), ATCC 68564, deposited Mar. 14, 1991.

5. A plasmid comprising genes coding for alcohol dehydrogenase and pyruvate decarboxylase, wherein said plasmid is capable of directing a gram negative host to produce alcohol dehydrogenase and pyruvate decarboxylase at a sufficient functional level to facilitate the production of ethanol as the primary fermentation product by said host.

6. The plasmid according to claim 5, wherein said plasmid comprises Zymomonas mobilis genes coding for alcohol dehydrogenase and pyruvate decarboxylase.

7. The plasmid according to claim 5, wherein said plasmid further comprises a lac promoter which directs the expression of said genes coding for alcohol dehydrogenase and pyruvate decarboxylase.

8. The plasmid according to claim 5, which has been designated pLOI555.

9. The recombinant host according to claim 1, comprising the plasmid pLOI555.

10. A method for the production of ethanol, comprising transforming an appropriate gram negative host, other than Escherichia coli, with heterologous genes coding for pyruvate decarboxylase and alcohol dehydrogenase, wherein said host expresses said genes at a sufficient functional level to facilitate the production of ethanol as the primary fermentation product by said host.

11. The method according to claim 10, wherein said host is selected from the group consisting of enteric bacteria.

12. The method according to claim 10, wherein said host is selected from the group consisting of Erwinia and Klebsiella.

13. The method according to claim 11, wherein said recombinant host has the ethanol producing characteristics of Klebsiella oxytoca M5A1(pLOI555) ATCC 68564, deposited Mar. 14, 1991.

14. A method for reducing the accumulation of acidic metabolic products in the growth medium of gram negative cells, said method comprising transforming said cells with heterologous genes coding for alcohol dehydrogenase and pyruvate decarboxylase, wherein said cells express said genes at a sufficient functional level to facilitate the production of ethanol as the primary fermentation product by said cells.

15. A gram negative recombinant host, other than E. coli, comprising a first heterologous DNA coding for alcohol dehydrogenase and pyruvate decarboxylase, respectively, wherein said host

(A) further comprises genes coding for proteins which enable said host to transport and metabolize an oligosaccharide, and

(B) expresses said genes and said first heterologous DNA at a level such that ethanol is produced as a primary fermentation product by said host from the metabolism of said oligosaccharide.

16. The recombinant host according to claim 15, wherein said host is selected from the group consisting of enteric bacteria.

17. The recombinant host according to claim 16, wherein said host is selected from the group consisting of Erwinia and Klebsiella.

18. The recombinant host according to claim 17, having the ethanol producing characteristics of

Klebsiella oxytoca M5A1(pLOI555), ATCC 68564, deposited Mar. 14, 1991.

19. The recombinant host according to claim 15, wherein said oligosaccharide comprises sugar monomers selected from the group consisting of C.sub.5 and C.sub.6 sugar monomers.

20. The recombinant host according to claim 19, wherein said oligosaccharide comprises sugar monomers selected from the group consisting of glucose and xylose.

21. The recombinant host according to claim 20, wherein said oligosaccharide is selected from the group consisting of dimers and trimers.

22. The recombinant host according to claim 15, wherein said host also produces a polysaccharase.

23. The recombinant host according to claim 22, wherein said host further comprises a second heterologous DNA segment, the expression product of which is said polysaccharase.

24. The recombinant host according to claim 23, wherein said polysaccharase is selected from the group consisting of a cellulolytic enzyme, a xylanoiytic enzyme, a hemicellulytic enzyme and a starch-degrading enzyme.

25. The recombinant host according to claim 22, wherein said polysaccharase is selected from the group consisting of an endoglucanase, cellobiohydrolase, .beta.-glucosidase, endo-1,4-.beta.-xylanase, .beta.-xylosidase, .alpha.-glucuronidase, .alpha.-L-arabinofuranosidase, acetylesterase, acetylxylanesterase, .alpha.-amylase, .beta.-amylase, glucoamylase, pullulanase, .beta.-glucanase, hemicellulase, arabinosidase, mannanase, pectin hydrolase, and pectate lyase.

26. The recombinant host according to claim 25, wherein said polysaccharase is an expression product of a gene selected from the group consisting of celD, xynZ, xylB, a .alpha.-amylase gene, and a pullulanase gene.

27. The recombinant host according to claim 26, wherein said celD and xynZ genes are derived from Clostridium thermocellum, said xylB genes are derived from Butyrivibrio fibrisolvens, said .alpha.-amylase gene is derived from Bacillus stearothermophilus, and said pullulanase gene is derived from Thermoanaerobium brockii.

28. The recombinant host according to claim 24, wherein said polysaccharase comprises the expression product of a cellulase gene of Cellulomonas fimi, and said host secretes at least some of said polysaccharase.

29. The recombinant host according to claim 23, wherein said host further comprises an additional heterologous DNA segment, the expression product of which is a protein involved in the transport of mono- and/or oligosaccharides into the recombinant host.

30. The recombinant host according to claim 23; wherein said polysaccharase is at least partially secreted by said host.

31. The recombinant host according to claim 23, wherein said polysaccharase is substantially accumulated in said host.

32. The recombinant host according to claim 31, wherein said polysaccharase is a thermostable enzyme.

33. The recombinant host according to claim 31, wherein said host further comprises an additional heterologous DNA segment, the expression product of which is a additional polysaccharase that is at least partially secreted by said host.

34. The recombinant host according to claim 33, wherein said different polysaccharase comprises the expression product of a cellulase gene of Cellulomonas fimi.

35. The recombinant host according to claim 1, wherein said host also produces a polysaccharase.

36. The recombinant host according to claim 35, wherein said host further comprises a second heterologous DNA segment, the expression product of which is said polysaccharase.

37. The recombinant host according to claim 36, wherein said polysaccharase is selected from the group consisting of a cellulolytic enzyme, a xylanolytic enzyme, a hemicellulytic enzyme and a starch-degrading enzyme.

38. The recombinant host according to claim 35, wherein said polysaccharase is selected from the group consisting of an endoglucanase, cellobiohydrolase, .beta.-glucosidase, endo-1,4-.beta.-xylanase, .beta.-xylosidase, .alpha.-glucuronidase, .alpha.-L-arabinofuranosidase, acetylesterase, acetylxylanesterase, .alpha.-amylase, .beta.-amylase, glucoamylase, pullulanase, .beta.-glucanase, hemicellulase, arabinosidase, mannanase, pectin hydrolase, and pectate lyase.

39. The recombinant host according to claim 38, wherein said polysaccharase is an expression product of a gene selected from the group consisting of celD, xynZ, xylB, a .alpha.-amylase gene, and a pullulanase gene.

40. The recombinant host according to claim 39, wherein said celD and xynZ genes are derived from Clostridium thermocellum, said xylB genes are derived from Butyrivibrio fibrisolvens, said .alpha.-amylase gene is derived from Bacillus stearothermophilus, and said pullulanase gene is derived from Thermoanaerobium brockii.

41. The recombinant host according to claim 38, wherein said polysaccharase is at least partially secreted by said host.

42. The recombinant host according to claim 38, wherein said polysaccharase is substantially accumulated in said host.

43. A method for treating an oligosaccharide feedstock, comprising the steps of

A. providing a feedstock that contains a starting oligosaccharide, and

B. bringing said feedstock into contact with an enzyme evolved by cells of a recombinant host according to claim 15, such that said starting oligosaccharide is acted upon by said enzyme.

44. A method according to claim 43, wherein said starting oligosaccharide is fermented to ethanol.

45. A method according to claim 44, wherein said starting oligosaccharide comprises a disaccharide or trisaccharide.

46. A method according to claim 43, wherein said enzyme is a polysaccharase and said starting oligosaccharide is converted by said polysaccharase to simpler oligosaccharides and/or saccharide monomers.

47. A method according to claim 46, wherein said starting oligosaccharide comprises a disaccharide or trisaccharide.

48. A method according to claim 46, wherein said starting oligosaccharide is an insoluble oligosaccharide selected from the group consisting of cellulose, hemicellulose and starch.

49. A method according to claim 48, wherein said polysaccharase is a heterologous polysaccharase.

50. A method according to claim 44, wherein said polysaccharase is a heterologous polysaccharase.

51. A method according to claim 46, wherein step B comprises heating said cells to induce lysis and release of said polysaccharase.

52. A method according to claim 51, wherein said starting oligosaccharide and/or said simpler oligosaccharides are fermented to ethanol.

53. A gram negative recombinant host, comprising a first heterologous DNA coding for alcohol dehydrogenase and pyruvate decarboxylase, respectively, wherein said host

(A) further comprises genes for the transport of an oligosaccharide and heterologous genes coding for proteins which enable said host to metabolize an oligosaccharide, and

(B) expresses said heterologous genes and said first heterologous DNA at a level such that ethanol is produced as a primary fermentation product by said host from the metabolism of said oligosaccharide.

54. A gram negative recombinant host, comprising a first heterologous DNA coding for alcohol dehydrogenase and pyruvate decarboxylase, respectively, wherein said host

(A) further comprises genes coding for proteins which enable said host to transport and metabolize an oligosaccharide selected from the group consisting of xylobiose, a trisaccharide and a long chain polysaccharide, and

(B) expresses said genes and said first heterologous DNA at a level such that ethanol is produced as a primary fermentation product by said host from the metabolism of said oligosaccharide.